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Invention: METHOD OF DETERMINING CLINICAL SEVERITY OF FALS

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Telephone: (202) 419-7000This is a:

- ☐ Provisional Application
- ☐ Regular Utility Application
- ☐ Divisional Application
- ☒ PCT National Phase Application
 - The complete disclosure of PCT/JP2004/018410, filed December 9, 2004 is incorporated by reference.
- ☐ Design Application
- ☐ Reissue Application
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SPECIFICATION

DESCRIPTION**Method of Determining Clinical Severity of FALS****Technical Field**

[0001] The present invention relates to a method for determining FALS based on interaction of NEDL1 and its associated factors with mutant SOD1, as well as a therapeutic agent and method therefor.

Background Art

[0002] Amyotrophic lateral sclerosis (ALS) is a neurodegenerative disease with poor prognosis, wherein muscular atrophy occurs by degeneration and deciduation of motor neurons of the spine, motor cortex and brainstem. Familial ALS (hereinafter, "FALS") is currently diagnosed among ALS patients at a frequency of 5-10%, and in some families the Cu/Zn superoxide dismutase (SOD1) gene is the gene responsible, with approximately 20% of FALS cases being attributed to mutations in the SOD1 gene. SOD1 is an active enzyme produced in cells during aerobic metabolism, and it inactivates the superoxide radical. The aggregate theory, which holds that mutated SOD1 (hereinafter referred to as "mutant SOD1") forms aggregates in cells and thereby exhibits cellular toxicity, has recently become the prevailing theory as the cause of FALS (Non-patent document 1).

[0003] Upon comparison between neuroblastomas with good prognosis and neuroblastomas with poor prognosis, the present inventors earlier discovered a novel HECT ubiquitin ligase, designated as NEDL1, whose expression is augmented in neuroblastomas with good prognosis (Patent document 1). It was also discovered that NEDL1 ubiquitinates mutant SOD1.

[0004] While much still remains to be learned about the intracellular transduction pathway of mutant SOD1, published reports have described the endoplasmic reticulum translocon component TRAP δ (translocon-associated protein complex), as a protein factor which binds solely to mutant SOD1 while not binding to normal SOD1 (wild-type SOD1) (Non-patent document 2, Non-patent document 3).

[0005] This interaction between mutant SOD1, produced by the causative gene for FALS, and its associated molecules are gradually being elucidated, but a full explanation of the mechanism of FALS pathology onset is still far in the future, even if the aforementioned aggregate theory is assumed to be correct.

[Patent document 1] International Patent Publication No. WO 03/018842

[Non-patent document 1] Nakano, R., Saibo Kogaku [Cell Technology], Vol.20, No.11, 1508-1512, 2001.

[Non-patent document 2] Ryen D. Fons, et al, The Journal of Cell Biology, Vol. 160, No. 4, 2003 (529-539)

[Non-patent document 3] Kunst C.B., et al, Nat. Genet. 15, 91-94 (1997)

Disclosure of the Invention

Problems to be Solved by the Invention

[0006] It has been a goal to elucidate the role of NEDL1 among interaction between mutant SOD1 and its associated peptides, and to verify the aggregate theory as the onset mechanism of FALS. The pursuit of this goal involving evaluation of binding and interaction between different molecules may provide knowledge leading to

improved treatment and diagnosis of FALS.

[0007] It is one object of the present invention to shed light on binding and interaction between mutant SOD1 and its associated molecules (whether or not mediated by NEDL1) at the genetic or protein level.

5 It is another object of the present invention to apply the acquired knowledge in the clinic, or in other words, to provide a novel therapeutic agent (and method) and diagnostic agent (and method) for FALS.

Means for Solving the Problems

10 [0008] The present inventors have found that NEDL1 binds to TRAP δ and that these form a complex with mutant SOD1, with a complex binding strength that is roughly proportional to the clinical malignancy of FALS. Similarly, it was found that NEDL1 also binds with Dishevell1 (hereinafter, "Dvl1") and that these form a complex with
15 mutant SOD1, with a complex binding strength that is roughly proportional to the clinical malignancy of FALS. Moreover, it was discovered that interaction between NEDL1 and mutant SOD1 is also roughly proportional to the clinical malignancy of FALS.

[0009] Specifically, there is provided a method for determining clinical
20 malignancy of FALS, characterized by isolating mutant SOD1 from a specimen taken from a FALS patient and evaluating the binding ability between the mutant SOD1 and TRAP δ .

[0010] There is further provided a method for determining clinical malignancy of FALS, characterized by isolating mutant SOD1 from a
25 specimen taken from a FALS patient and evaluating the binding ability between the mutant SOD1, and NEDL1 and Dvl1.

[0011] There is still further provided a method for determining clinical malignancy of FALS, characterized by isolating mutant SOD1 from a specimen taken from a FALS patient and evaluating the binding ability between the mutant SOD1 and NEDL1.

5 [0012] That is, the present invention provides the use of NEDL1 or its substrate for determination of clinical malignancy of FALS. The determination is characterized specifically by the use of isolated mutant SOD1. The aforementioned substrate is preferably TRAP δ or Dvl1.

10 [0013] In addition, there is provided an inhibitor of interaction between mutant SOD1 and NEDL1 and/or its substrate.

[0014] The aforementioned substrate is preferably TRAP δ or Dvl1.

15 [0015] There is even further provided a method of screening for agents that are useful for treatment of FALS, characterized by determining whether or not a candidate drug is an inhibitor against interaction between mutant SOD and NEDL1 and/or its substrate in neurons.

Effect of the Invention

20 [0016] According to the present invention, it has been demonstrated that complexes are formed between mutant SOD1, which is a causative gene of FALS, and its associated molecules (TRAP δ , Dvl1, etc.) through NEDL1, and the aggregate theory for the onset mechanism of FALS has been confirmed. Furthermore, since the binding ability between mutant SOD1 and the aforementioned molecules in such complexes (whether or not mediated by NEDL1) are associated with clinical malignancy of FALS, it is possible to determine the clinical malignancy of FALS based on evaluation of the binding ability.

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[0017] Inhibiting formation of the aforementioned aggregates may

contribute to treatment of FALS. According to the invention, therefore, there are provided inhibitors of interaction between mutant SOD1 and NEDL1 and/or its substrate, which should be useful for treatment of FALS.

5 **Brief Description of the Drawings**

[0018] Fig. 1 shows a conserved amino acid sequence alignment for human NEDL1 (hNEDL1) and mouse NEDL1 (mNEDL1). The numbers at right represent the amino acid numbers counting from the initiator methionine. The C2 domain, WW domain and HECT domain are all indicated.

Fig. 2 is an electrophoretogram (immunoblot diagram) showing an immunoblot of binding between NEDL1 and TRAP- δ .

Fig. 3 is an electrophoretogram showing an immunoblot of binding between NEDL1 and endogenous TRAP- δ .

15 Fig. 4 is an immunoblot diagram showing binding between NEDL1 and mutant SOD1.

Fig. 5 is an immunoblot diagram showing ubiquitination of wild-type SOD1 and mutant SOD1 by NEDL1.

20 Fig. 6 is an immunoblot diagram showing time-dependent change in degradation of mutant SOD1 and wild-type SOD1 in the presence of NEDL1.

Fig. 7 is an immunoblot diagram showing binding between mutant SOD1 and exogenous TRAP δ .

25 Fig. 8 is an immunoblot diagram showing binding between NEDL1 and Dvl1.

Fig. 9 is an immunoblot diagram showing ubiquitination of Dvl1 by

NEDL1.

Fig. 10 is an immunoblot diagram showing time-dependent change in Dvl1 degradation in the presence of NEDL1.

Fig. 11 is an immunoblot diagram showing binding between mutant SOD1 and Dvl1 in the presence of NEDL1.

Fig. 12 is a schematic diagram showing the interaction between mutant SOD1 and its associated molecules in onset of FALS pathology.

Best Modes for Carrying Out the Invention

[0019] The present invention will now be explained in greater detail with respect to preferred modes.

[0020] The NEDL1 gene with which the present invention is concerned is a gene with a total length of 6200 bases (4775-base coding region), and its nucleotide sequence is listed as SEQ ID NO: 2 of the Sequence Listing. The NEDL1 protein encoded by the gene comprises 1585 amino acids, and its full length sequence is listed as SEQ ID NO: 1 of the Sequence Listing. The aforementioned nucleotide sequence and amino acid sequence have been registered with GenBank (<http://www.ncbi.nlm.nih.gov>) as Accession No. AB048365.

[0021] Fig. 1 shows an alignment (homology analysis) for human NEDL1 (hNEDL1) and mouse NEDL1 (mNEDL1). The NEDL-1 protein has the following domains, with HECT ubiquitin ligase features. Specifically, these are (1) an N-terminal C2 domain (which calcium-dependently binds to membrane lipids), (2) a middle WW domain (which contributes to binding with proline-rich regions) and (3) a C-terminal HECT domain (the binding site of ubiquitin-conjugating

enzyme E2).

[0022] For identification of NEDL1 substrates, the present inventors used the aforementioned WW domain (positions 757-1114) for yeast two hybrid screening. As a result, TRAP δ was discovered as one substrate thereof.

[0023] TRAP δ is one constituent protein subunit of translocon-associated protein complex, which is a factor associated with translocation of proteins crossing the endoplasmic reticular membrane. It has already been reported that TRAP δ does not bind wild-type SOD but does bind mutant SOD1 (Kunst C.B. et al., cited above). The present inventors therefore examined interaction between NEDL1, TRAP δ and SOD1. Specifically, we co-transfected COS7 cells with their expression constructs and performed analysis by immunoblotting and immunoprecipitation assay.

[0024] Binding between NEDL1 and TRAP δ

The analysis resulted in confirmation that NEDL1 binds to both endogenous and exogenous TRAP δ , as shown in Figs. 2 and 3. This binding was also confirmed by yeast two-hybrid screening to be through the aforementioned WW domain. However, TRAP δ is not ubiquitinated by NEDL1.

[0025] Binding between NEDL1 and SOD1

The aforementioned analysis also resulted in confirmation that NEDL1 binds to mutant SOD1 but not to wild-type SOD1, as shown in Fig. 4. Moreover, the binding ability between NEDL1 and various mutant SOD1 molecules is seen to be roughly proportional to clinical malignancy of the FALS patients from which the mutant SOD1

molecules are isolated.

[0026] In addition, it was confirmed that NEDL1 ubiquitinates mutant SOD1 (Fig. 5), and that the degree of ubiquitination is roughly proportional to clinical malignancy of the FALS patient from which the mutant SOD1 molecule is isolated.

[0027] Fig. 6 shows time-dependent change in degradation of mutant SOD1 in the presence of NEDL1, and here as well it is seen that mutant SOD1 is degraded in proportion to clinical malignancy.

[0028] These results indicate that NEDL1 mediates degradation of mutant SOD1 through ubiquitination, and that degradation proceeds in proportion to clinical malignancy.

[0029] Binding between TRAP δ and SOD1

The aforementioned analysis also resulted in confirmation that exogenous TRAP δ binds to mutant SOD1 but not to wild-type SOD1, as shown in Fig. 7. As in the case of NEDL1, the binding ability between TRAP δ and various mutant SOD1 molecules is seen to be roughly proportional to clinical malignancy of the FALS patients from which the mutant SOD1 molecules are isolated.

[0030] To summarize these and other research results, the role of NEDL1 in onset of FALS pathology is presumably the following: (1) NEDL1, either alone or with TRAP δ , ubiquitinates mutant SOD1; (2) NEDL1 and TRAP δ form aggregates with mutant SOD1, which induce fragmentation of the Golgi apparatus and lead to apoptosis of neurons; (3) aggregate formation is responsible for loss of NEDL1 and/or TRAP δ function, producing a condition associated with motor neuron death; and (4) NEDL1/TRAP δ /mutant SOD1 aggregates are taken up

and inactivate factors such as molecular chaperones whose normal functioning is important to motor neuron survival.

[0031] Next, in order to identify the NEDL1 substrate during ubiquitin-dependent proteolysis, the present inventors performed yeast two hybrid screening using a separate domain of NEDL1 containing the WW domain (positions 382-1448). As a result, Dvl1 was identified as the substrate.

[0032] Human DV11 is a protein comprising 670 amino acids, with the following domains. Specifically, these are (1) the DIX domain required for canonical Wnt/TCF signaling, (2) the PDZ domain (target of Stbm, CKI binding) and (3) the DEP domain (involved in membrane localization during PCP signaling) (D.J. Sussman et al., Dev. Biol. 166, 73-86 (1994); A. Wodarz et al., Cell Dev. Biol. 14, 59-88 (1998); M. Boutros et al., Cell, 94, 109-118 (1998)), and it is believed that the DEP domain binds with the NEDL1 WW domain.

[0033] The interaction between NEDL1, DV11 and SOD1 was examined, in the same manner as for TRAP δ . Specifically, we co-transfected COS7 cells with their expression constructs and performed analysis by immunoblotting and immunoprecipitation assay.

[0034] Binding between NEDL1 and Dvl1

The aforementioned analysis resulted in confirmation that NEDL1 binds Dvl1, as shown in Fig. 8. It was also confirmed that NEDL1 ubiquitinates Dvl1 (Fig. 9), and Fig. 10 shows time-dependent change in degradation of Dvl1 in the presence of NEDL1.

[0035] Binding between Dvl1 and SOD1

The aforementioned analysis resulted in confirmation that Dvl1 binds

SOD1 in the presence of NEDL1, as shown in Fig. 11. Moreover, the binding ability between Dvl1 and various mutant SOD1 molecules is seen to be roughly proportional to clinical malignancy of the FALS patients from which the mutant SOD1 molecules were isolated.

5 [0036] Motor neuron cytoskeleton abnormalities have been reported in ALS patients, suggesting that the influence of the aforementioned mutant SOD1 molecules on NEDL1-mediated Dvl1 degradation may contribute to motor neuron death (Luo, Z.G. et al., Neuron 35, 489-505 (2002)).

10 [0037] Conclusion

The neuronal E3 ubiquitin ligase NEDL1 binds (interacts with) TRAP δ but also binds Dvl1, ubiquitinating and degrading it. Since NEDL1 thus forms complexes with mutant SOD1, Dvl1 and TRAP δ , it forms large aggregates particularly with mutant SOD1 molecules that have
15 escaped ubiquitin-mediated degradation. The function of NEDL1 that affects the activity of the target protein (substrate) Dvl1 or TRAP δ is regulated by mutant SOD1. All of these individual interactions are connected with onset of FALS pathology. Thus, elucidation of the molecular mechanisms by which these complexes or large aggregates
20 are formed will shed light on motor neuron death in ALS and should thus lead to promising new therapeutic agents and methods for ALS. Fig. 12 is a schematic diagram showing the interaction between mutant SOD1 and its associated molecules in onset of FALS pathology, based on knowledge obtained according to the present invention.

25 [0038] FALS therapeutic agent and treatment method

In light of the aforementioned considerations, the present invention

provides inhibitors against interaction between mutant SOD1 and NEDL1 and/or its substrate. Candidate drugs that are potentially useful as inhibitors include nucleic acids, proteins, low molecular compounds (chemically synthesized or naturally derived), and polymer compounds other than proteins.

[0039] As a screening method for such inhibitors there may be mentioned the Two-Hybrid System (for example, Gyuris, J. Cell, 1993, 75, 791-803; Golemis, E. A., Current Protocols in Molecular Biology (John Wiley & Sons, Inc.) 1996, Ch. 20.0-20.1). The inhibitor screening method may also be carried out by an immunological method. Specifically, after expressing a mutant SOD1 (especially one associated with high clinical malignancy) and NEDL1 and/or its substrate in cells (neurons) and culturing the cells for a fixed period with the candidate drug, the cells are crushed to prepare a cell lysate. By immunoprecipitating one molecule with an antibody and detecting or quantifying the other (different) molecule in the precipitate using an immunological method, it is possible to detect the effects of candidate drugs on the interaction of each molecule. Screening of inhibitors is also possible by simultaneously adding an appropriate agonist with the candidate drug to the culturing system and performing the aforementioned assays, and then comparing this with immunoprecipitate from cells containing no candidate drug.

[0040] The protein or other inhibitor of mutant SOD1 and NEDL1 and/or its substrate, once identified by the aforementioned screening method, is then orally or parenterally administered to a patient suffering from or suspected of suffering from FALS. The protein is

formulated as a pharmaceutical preparation for this purpose. An appropriate dosage form is prepared by combining an effective dose of the binding inhibitor with a pharmaceutically acceptable carrier or diluent. Dosage forms suitable for administration include tablets, pills, powders, solutions, suspensions, emulsions, capsules, suppositories, injections and the like.

Examples

[0041] (Method)

(Cloning of human NEDL1 cDNA)

10 Cloning of human NEDL1 cDNA is described in detail in International Patent Publication No. WO 03/018842 (PCT/JP02/08524), but for the present invention it was carried out in the following manner. Specifically, a forward primer (5'-GGTTTTTAGGCCTGGCCGCC-3', SEQ ID NO: 3) and a reverse primer (5'-
15 CAATGAGGTACATGCCAATCC-3', SEQ ID NO: 4) were used for amplification of the 5' portion of NEDL1 cDNA (from a human neuroblastoma cDNA library) with human fetal brain (Stratagene) as template. Full-length human NEDL1 cDNA was constructed by fusing the PCR-amplified fragment (nucleotide positions 1 (translation
20 start codon) to 68) with KIAA0322 cDNA (donated by T. Nagase of Kazusa DNA Research Institute).

[0042] (Cell culturing and transfection)

The cells were grown in RPMI1640 medium containing 10% heat-inactivated fetal bovine serum (FBS, Life Technologies, Inc.),
25 penicillin (100 IU/ml) and streptomycin (100 µg/ml). COS7 and Neuro2a cells were maintained in Dulbecco's modified Eagle medium:

DMEM) containing 10% heat-inactivated fetal bovine serum and penicillin (100 IU/ml)/streptomycin (100 µg/ml). The cells were cultured at 37°C in an atmosphere of moisture-saturated air with 5% carbon dioxide gas. The co-transfection of each expression plasmid was accomplished using LipofectAMINE (Life Technologies, Inc.) according to the manufacturer's instruction manual. For some experiments, the transfected cells were treated for 30 minutes with MG-132 at a final concentration of 40 µM.

[0043] (Yeast Two-Hybrid Screening)

The screening was carried out using a Gal4-based matchmaker two-hybrid system (Clontech) with a cDNA library obtained from human fetal brain (primary screening) and human adult brain (secondary screening). *Saccharomyces cerevisiae* CG1945 cells were transformed with pAS2-1-NEDL1-1 (positions 757-1114, primary screening) or pAS2-1-NEDL1-2 (positions 382-1448, secondary screening). Both of these expression vectors fail to activate only LacZ transcription. The transformants were further transformed with the aforementioned cDNA library. LacZ-positive colonies were selected. Plasmid DNA was extracted from the positive colonies and the nucleic acid sequence was determined.

[0044] (*In vitro* ubiquitination assay)

An *in vitro* ubiquitination assay was conducted in the following manner. There were incubated 0.5 µg of purified GST fusion protein, 0.25 µg of yeast E1 (Boston Biochem), 1 µl of crude cell lysate from E2s-expressing *E. coli* and 10 µg of bovine Ub (Sigma) in 250 mM Tris-HCl (pH 7.6), 1.2 M NaCl, 50 mM ATP, 10 mM MgCl₂ and 30 mM

dithiothreitol. After 2 hours at 30°C, SDS sample buffer was added to suspend the reaction. The sample was analyzed by SDS-PAGE, transferred to a membrane and immunoblotted with anti-ubiquitin monoclonal antibody (Medical Biological Laboratories).

5 [0045] (Expression construct)

A hemagglutinin-tagged and His6-tagged mammalian ubiquitin expression plasmid was donated by D. Bohmann. The full-length NEDL1 cDNA was introduced into the mammalian expression plasmid pEF1/His (Invitrogen) or pIRESpuro2 (Clontech). cDNA coding for
10 wild-type or mutant SOD1 was linked to the carboxyl terminal of FLAG or Myc epitope tag sequence and subcloned in pIRESpuro2. FLAG or Myc epitope tag was also linked to the carboxyl terminal of TRAP δ . FLAG or Myc epitope tag was also linked to the amino terminal of Dvl1. The coding sequence was confirmed using an
15 automatic DNA sequencer.

[0046] (Immunoprecipitation and Western blotting analysis)

Anti-NEDL1 antibodies and anti-TRAP δ antibodies were prepared in rabbits against NEDL1 oligopeptide (positions 460-482) and TRAP δ oligopeptide (positions 93-126). In an immunoprecipitation
20 experiment, COS7 cells or Neuro2a cells were co-transfected using the expression plasmids in different combinations. After 48 hours, the cells were lysed in TNE buffer (10 mM Tris-HCl pH 7.8, 150 mM NaCl, 1% NP-40, 1 mM EDTA, 1 mM PMSF) containing a protease inhibitor cocktail (Sigma). The whole cell lysate was
25 immunoprecipitated using anti-NEDL1 antibody, anti-FLAG antibody (M2, Sigma) or anti-Myc antibody (9B11, Cell Signaling Technology).

The immune complexes were recovered on GTP-binding protein Sepharose beads and boiled in Laemmli sample buffer for elution, electrophoresed on SDS polyamide gel and then transferred to a polyvinylidene difluoride membrane (Immobilon, Millipore) by electroblotting. In a ubiquitination experiment, cytolysis was carried out in RIPA buffer (10 mM Tris-HCl pH 7.4, 150 mM NaCl, 1% NP-40, 0.1% sodium deoxycholate, 0.1% SDS, 1 mM EDTA) and subsequently subjected to high power ultrasonic treatment. The membrane was probed with a first antibody, and then incubated with a second antibody labeled with horseradish peroxidase (Jackson ImmunoResearch Laboratories/Southern Biotechnology Associates, Inc.). The immunoreactive band was detected by ECL enhanced chemiluminescence (Amersham Pharmacia Biotech). In a proteolysis experiment, Neuro2 cells were transfected with a prescribed expression plasmid. At 48 hours after transfection, the cells were treated for a prescribed time with 50 µg/ml of cycloheximide (Sigma). An equivalent of whole cell lysate (50 µg) was then subjected to Western blotting and quantified using Intelligent Quantifier software (Bio Image).

[0047] (Example 1) Binding between NEDL1 and TRAPδ

COS7 cells were co-transfected with the expression plasmids shown in Fig. 2 (NEDL1 and FLAG-TRAPδ). The whole cell lysate was immunoprecipitated (IP) with anti-FLAG antibody (first panel) or anti-NEDL1 antibody (second panel). The immunoprecipitate was subjected to immunoblotting (IB) using the antibodies shown in the figure. The whole cell lysate was subjected to immunoblot analysis

for expression levels of each protein (third and fourth panels). Detection was accomplished using secondary antibody conjugated with horseradish peroxidase. COS7 cells were also transfected with xpress-NEDL1 expressing plasmid for a similar experiment (Fig. 3).
5 The results confirmed binding between NEDL1 and TRAP δ , for exogenous TRAP δ .

[0048] (Example 2) Binding between NEDL1 and mutant SOD1

Whole cell lysate from COS7 cells overexpressing NEDL1 and FLAG-tagged mutant SOD1 or wild-type SOD1 was immunoprecipitated
10 using anti-FLAG antibody (first panel) or anti-NEDL1 antibody (second panel), and then immunoblotted using anti-NEDL1 antibody or anti-FLAG antibody. Expression of NEDL1 or FLAG-tagged mutant SOD1 was analyzed using anti-NEDL1 antibody (third panel) or anti-FLAG antibody (fourth panel) (Fig. 4). Here it is seen that mutant
15 SOD1 (C6F, A4V) binds strongly with NEDL1 when onset is followed by a rapid clinical course leading to death of the patient within 1.5 years (Fig. 4, lanes 3,4). On the other hand, there is virtually no binding of mutant SOD1 (L126S, H46R, D90A) with NEDL1 when onset is followed by a slower clinical course (Fig. 4, lanes 11-13).
20 The mutant SOD1 (G93A) which exhibits unique nerve symptoms after onset binds moderately with NEDL1. Also, it is seen that wild-type SOD1 and NEDL1 do not bind (no co-precipitation) (lane 2).

[0049] (Example 3) Binding between TRAP δ and mutant SOD1

COS7 cells were transiently co-transfected with an expression plasmid
25 coding for FLAG-tagged TRAP δ and Myc-tagged mutant SOD1 or Myc-tagged wild-type SOD1. Whole cell lysate was

immunoprecipitated using anti-Myc antibody (first panel) or anti-FLAG antibody (second panel), and then immunoblotted using anti-FLAG antibody or anti-Myc antibody. Expression of FLAG-tagged TRAP δ or Myc-tagged mutant SOD1 was analyzed using anti-FLAG antibody (third panel) or anti-Myc antibody (fourth panel). Here it is seen that mutant SOD1 (A4V) binds strongly with TRAP δ when onset is followed by a rapid clinical course leading to death of the patient within 1.5 years (Fig. 7, lane 4). On the other hand, virtually no binding of mutant SOD1 (H46R) with TRAP δ occurs when onset is followed by a slower clinical course (lane 6). Also, it is seen that wild-type SOD1 and TRAP δ do not bind (no co-precipitation) (lane 3).

[0050] (Example 4) NEDL1-dependent ubiquitination

NEDL1 ubiquitinates mutant SOD1 in a manner dependent on the type of SOD1. COS7 cells were transiently co-transfected using the expression plasmids shown in Fig. 5. Whole cell lysate from the transfected COS7 cells was immunoprecipitated with anti-Myc antibody, and immunoblotted using anti-ubiquitin antibody (upper panel). The degree of ubiquitination was roughly proportional to the clinical malignancy of FALS (A4V>G93A>H46R). Whole cell lysate was immunoblotted with anti-NEDL1 antibody to confirm expression of the transfected NEDL1 (lower panel). In this photograph, arrows indicate the positions of non-ubiquitinated SOD1, and the molecular weight marker positions are shown at left.

[0051] (Example 5) Half-life of wild-type SOD1 and mutant SOD1 in the presence and in the absence of NEDL1.

Lysates of Neuro2a cells transfected with blank vector or NEDL1

expression plasmid, recovered at different time points after addition of cyclohexidine (final concentration: 50 µg/ml) as shown in Fig. 6, were immunoblotted with anti-FLAG antibody for analysis of SOD1 protein levels. Mutant SOD1 was more rapidly degraded than wild-type SOD1. NEDL1 did not affect degradation of wild-type SOD1. It is seen that degradation of mutant SOD1 protein is accelerated and the half-life of mutant SOD1 protein in the presence of NEDL1 decreases roughly in proportion to the severity of FALS (A4V>G93A>H46R).

[0052] (Example 6) Binding between NEDL1 and Dvl1

Myc-tagged Dvl1 was overexpressed with NEDL1 in COS7 cells. Whole cell lysate was immunoprecipitated with anti-NEDL1 antibody and then immunoblotted using anti-Myc antibody (upper panel of Fig. 8). The expression level of Myc-tagged Dvl1 was analyzed by immunoblotting using anti-Myc antibody (lower panel).

[0053] (Example 7) NEDL1-dependent ubiquitination of Dvl1

NEDL1 ubiquitinates Dvl1 in COS7 cells. COS7 cells were transiently co-transfected using the expression plasmids shown in Fig. 9. Whole cell lysate from the transfected COS7 cells was immunoprecipitated with anti-Myc antibody, and immunoblotted using anti-ubiquitin antibody (upper panel). The whole cell lysate was immunoblotted with anti-xpress-NEDL1 antibody (middle panel) or anti-Myc antibody (lower panel), to confirm expression of the transfected NEDL1 or Myc-Dvl1.

[0054] (Example 8) Degradation of Dvl1 by NEDL1

Neuro2a cells were transfected using FLAG-tagged Dvl1 expression plasmid, in the presence or in the absence of NEDL1-expressing

plasmid. The transfected cells were recovered at different time points after addition of cyclohexidine (final concentration: 50 µg/ml), as shown in Fig. 10. Neuro2a cell lysate was immunoblotted with anti-FLAG antibody for analysis of the Dvl1 protein level. The half-life of FLAG-Dvl1 was notably reduced in the presence of NEDL1.

[0055] (Example 9) Binding between Dvl1 and mutant SOD1

COS7 cells were transiently co-transfected using the expression plasmids shown in Fig. 11. Whole cell lysate was immunoprecipitated with anti-Myc antibody and then immunoblotted using anti-FLAG antibody or anti-Myc antibody. It is seen that binding between Dvl1 and mutant SOD1 is enhanced in the presence of NEDL1 (Fig. 11, lane 4). The binding ability decreased roughly in proportion to the severity of FALS (A4V>G93A>H46R).

Industrial Applicability

[0056] As explained above, the present invention allows determination of clinical malignancy of FALS patients from which mutant SOD1 has been isolated, by evaluating binding ability between NEDL1 and the mutant SOD1 or by evaluating binding ability between NEDL1-associated factors and the mutant SOD1 either in the presence or absence of NEDL1, and it is therefore useful for diagnosis of FALS.